

unaited

```

; Sequence 2, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
; APPLICANT: Dror I. Baruch
; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidlig
; APPLICANT: Jurg Gysin
; APPLICANT: Bruno Pouvelle
; APPLICANT: Nobutaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; TITLE OF INVENTION: (PEEMP1) THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087,013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-2
MGFSCKYFLIKMGNAASLEGDAKSPITIKESHKARNVLEYAKNIRHPSKYAKEHVDLSKGLDT
KAEFRGSPSTPVNKNHYVYPICNDLKHETHNLRYDQVNLRRHCHRGEDNREDESECGNKIR
NYKRNDAJACAPRRRHCDNLKLEALNDINTONHIDLGNLYLTKAYGESIVNNHPRKGTSDA
CTALASFPADIGIVAGIDMEKPNYADKREYGTGLREVEYKIHGMEDEVKNDYNDPSGNGVYKRE
AMNVRNKNVMAICDIAICDASGYEPMOSBSNTPLESNPKCKCKGCVPTNDYVYPLRPDEMG
BERCRRNRIKLVKVDSCNDRERLYCSHNGHDCITTTIRKGLIHLNCKTDCSTCKAYEVLG
NOQEARCKOKEREYKEIYSYLNDNKEVNNINSEYKQYERKLEQYATNDTFLNLNLEGYCK
GGJPGKEDJTFNNSADCKGIFYRESCQVPCGVKCDGIKYTHKSDNDRERNEDYPRPWGK
PNITIVLYSGNQGDTOKLENNFNSSTNYKDNNOQMECYKDEINRCKLEONTEINNDPKI
ISEHNEFELWVLYLADDTIKMNDKLTCTINNTHHCIDECNRNCLCFDRWVOKKEEEMSIKLE
TKKNTQOSVYSGNINLPGFYPRKVDKLDKDEAKKELMENIKRKNFESNLNNRDLNENALIE
LLDLHLEKATYICKDNNTBACETSNNATNCPVPRGCTOPTKNIKETAQYFKRSAYEARNNG
LHRLKGAHEGILYKRGGRKDERDNLCRIMIKHSNKNLGSNGPCDCKGTGDIQTRFVGTWE
VDPENHKKHEDVIMPERRRHICTSNLEJQTDHDLNGNIVDLYNNSFLGIVLLSAKYEANKI
IMYERKNLKGPK EYTDHOTTICRAIRSEFADIGDIIRGDLERNRGNMVKLOGHLETVGN
IKHSLKGNNDYNDAPYKYLREMMWEMANRAKWEAMKCDIKYILDKRSGHOSOTSYCGSDH
TPLDVIYPOKLRMMTEMAMWYCKVOK EYDKLEKCKECKDCKGCTKESGCTGCTKEACNE
YNDIIGJMKKEONNIIISDKTELHEBQKMSVNSGIEASSTAKNHNDRNITELSELVQNGKSN
KGSISDESAVIGTNTTYENVGAYLHDTGNFDDCQSONEFCDKSDGKNEKYAFROKPDHGDAC
GCKSGSKPRVQIKTKRKAEBEDTBCITVNDILKENDKQYEDCHPKRNSNGYPMOCGNILY
EDPRVCMPPRRQKLVHFLANDNEIKLQSOVNLKPAFIRKSAAEFFSMYYKSKGEGNELDK
ELKEGKIPRAPLRSMFTYTGDRDPLFGTDISKGHEGSKLEQIDSLFKNDOCKSPNGKTRQEW
WHEHSEHTEAMLCALVYKIGAKKDDPTENVYNNYKFSKSPSTIEFAKRPOTLRNLTWYDNC
YTRQKYLKVQEKCSNDOLKCDTEBCKNCKEDYVYIMKKKKETIPDDKTYKDERDKRFRDROHIG
VAVDTGTINADIVYLRKRTYASCGKPGSASVAVORNIQLLEKQAYYADAKHCGCTKEIENDKYT
NISKDKCGLVKEANTGALIKWNGPNPNYNNLKELEDEYLFPSRLRICFHALDGNYPDEYKD
ENGLRRLMEVATBEGYNLGOYKKEKKEKIKTSDAKSYEVPSCSAMKYSFYDLRIDILIGID
NLEDEKOTKEENLKIENKNGTSVSGSDSTGNPSTARKFEMNENKECVNMAMICVGRGRDD
GNSGNSARSEDELKKGVSPPDDDYPMGKNRDEGTAYOPLRMPAEWGEDCKHKEKELEKIVGAC
NDYTCGDNDRKCKKCTDACTQYKKTISEMKPOYKOKIKYGENKDKIYSEHYAKADADAREYLD
KOLUKICEKNSDCEYCKKADYSTOLCTDGNSONPASLDDPEKVEGKNCQVPRGPPRARET
PSPRVSILKATASKEAKTAPPTKQPKVENLJTEMRAQOTRTARRAQQTRKRTSTATTESDVG
TAVKALISNKPDSRGIEGNCNPKTYGOYPRKGCIVKSKENNGIOMPPRRKLCINNTIOYLANE
TENKRRNDIKKEAFIKCALETOTFLMKYIIEENPAENLONGTIPEEFKIMVYTYGDKDMFEG
TQISNDKLIITYNSVTTLINNNKKKODKKKDEDELKTFEMKNNKFTWEGMAYGLTYVHLTDENE
KEKIRBNVOYNDMTKITPSELEVKRPQPLRMTPEWAEEFCNKRKQSLKLEAGCKEYECNSND
GTQOBEACVYTONITKMKTEYERQREKFKDKDKGRKYKDYPTSERDIEKATCAHEYLNNMLK
ELCGNDCSCMOPSSOLKPTTQOOSQSDANDPESLIDVPEFNKCECPBELSKGSMITRKIT
BKRIIPNDCVKAAYLYLSKEANNMDITLKEKFIPIESTKEKSKNSMTNNPCDPKPPYAPDKYI
GRNPNCEENRENEFKYVDEMKCYKNSKFQOEKKRVCPPRPREMKLRNLDEIKIERLKDXYLLK
NVBRTRANGIDITIKNFENSEGAMPICDTMTKYSFADIGDIYRGDMLRIGGILPRAVEIKLYV
FEYIYKGMKNNKGRKRYNDVOTFRSAGANDAKRDKWKAMTKCAPEDAKLFRKGRMDGFERITLI
ORCKGKDDPPYVDYTIPOFRMNTWSEYCYKALMELEKFKSCHCKTSDCKNDYENKCEQ
CTKCOEYKFNVLKMWKSLFDIQSNKYKELYEQPIYTKISTYHVNQFVQKLATFSECSVESFSE

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YLHETSKCLNRYKENENDGSSNIRTYAFEEETPKSYKACSCQLPSKNPLDNCPTDQNKDCKELQ
FTFCSKNDYNDNLDNNALYLINSSSDNKGVLIPRRRHLCRTPITAYNVRKGDKEILKCKLITS
AFSOGOLGOKYKSEELCEFEAMKYSADYSDIIGTDMNDTSLSKIKYIFETSSEATENRKTW
WENNRQIYHAILCCKIKITSKYTLDEGCOQLPKDEETNOPLRMLIEMAKOACKEKHHVSDISKT
KCPRSNEDNEFASSELIRPGCCONDITRTYISLNTLKNMENLNTKQULKDOSSGNIDNKPSEEN
VOSYIKSKDSOCALENDINEJVTGTRNNNEFEKVELKLYGLYFVDETHKNNVLDGNLKEE
EOTVRKALYFFTPHYDSFYQALFSTHRVAQDPKNDILKSSISVYISALGLILALHPMKKFKF
SSVDLRLINIPQEGEMPTLESKNRYIYRSGPYKGTIYMEGDSGDEKYMMDLSSDITS
SESEYELDINDIYVPGSPRYKTYLLEVYLEPSKROIPSDTPSNDTPRNTFRITDDEMNELKHDFV
SOLYPRTEPNNNYKSADIPMNTEPNLTYSNDNPEKPFITISINDROLYTGKEISYININMSTNTNND
LPMNANDSYRGIDLINDSLVVLNLLIYMKKI1

```

```
; Sequence 3, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
; APPLICANT: Benoit Gamain
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; APPLICANT: Pierre Buffet
; APPLICANT: Christine Scheidig
; APPLICANT: Jurg Gysin
; APPLICANT: Bruno Pouvelle
; APPLICANT: Nobutaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1 THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; CURRENT APPLICATION NUMBER: US/10/087,013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-3
EAEKELEKGIPEGFRQMFYTFGDRDILEGI
```

```
; Sequence 4, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
; APPLICANT: Louis H. Miller
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; APPLICANT: Nobutaka Fujii
; APPLICANT: Joseph Smith
; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1 THAT MEDIATES ADHESION TO CHONDROITIN SULFATE A
; CURRENT APPLICATION NUMBER: US/10/087,013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-4
KELKEKGIPEI
```

PEPB = residues 1279-1554 of Seq ID # 2

```
; pepb.pep
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
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; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087,013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
PEPB.PEP
DCHPKNSNGYPPDQCGNINVEDEPRVCMPPRRORLQVHFLANDNEIRKLSQVNLKEAFIKSAAEITFF
SMYYKSKDGEENELDKELKESKIPPAFLRSFYFGDYRDLFGTIDISKHGEESKLEOIDSLEKNGD
OKSPNGKTRQEMTEHSEIWEAMLCALVKIGAKDDFTENYGYNNVKSXSDSTLLEEFARPOELRWLT
EMYDQCYTRQKYLKDVQEKCKNSQGLCDTECNKCKEDYKMKKKKKEMIPDKYYKDEKDKKRF1
```

276

res: dno

PEPA = residues 403-747 of SEQ ID 2

```
; Sequence 2, Application US/10087013
; GENERAL INFORMATION:
; APPLICANT: Arthur Scherf
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; TITLE OF INVENTION: IDENTIFICATION OF THE DOMAIN OF
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM ERYTHROCYTE MEMBRANE PROTEIN 1
; FILE REFERENCE: NIH176.001C1
; CURRENT APPLICATION NUMBER: US/10/087, 013
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/US00/24195
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152, 023
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3542
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-087-013-2
YEKIQSYLSNDNKFVNNINSEYKQFYEKIKETQVATNDTEFLNLNEGKYCKGGLPGKDDITFTNSADD
KGIETRESEYQVDCGKCDGKITYTRKSDNDRERVNNEDYKPPWGVKPTNITVLYSGNNEGDIITOKLEN
FCNSSTYKDKNNQKWCYKNDKINRCKLEQNTREINNDNPKIISFHNFEELAVTYLLRDTIKWDDKIKT
CINNTTTCIDECNRNCICFDRWVKOKEEWNSIKLFTKKNNIQOSYSNINNLFGYEFKKVMDKIDKD
EAKKEIEMENIKRKKNFESNENNRDYLENAIELLDHLEKATICKDNNNTNENACETSHNATTNP1
```

345

residues

> 0 <
0110 Intelligenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file pep1.res made by shanley on Tue 24 Jun 103 8:58:54-PDT.

Query sequence being compared: US-10-087-013-2 (1-345)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-10-087-013-2 (1-345) with:
File: pep911.pep

```

100-
N -
U 50-
M -
B -
E -
R -
O 10-
S -
E 5-
O -
E -
N -
E -
S -
E -
C -
E -
S 0-
SCORE 01 1 2 13 4 1 6 7 1 8 1 9 10
STDDEV -4 -3 -2 -1 0 1

```

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 6
Randomization group 0

SEARCH STATISTICS

Scores: Mean 8 Median 8 Standard Deviation 1.73
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 970
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

PEPA vs Seqs 9-11

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame
1. US-10-087-013-10 Sequence 10, Application US/10087013	*** 1 standard deviation above mean *** *** 0 standard deviation from mean ***	311	10	49	1.15	0
2. US-10-087-013-11 Sequence 11, Application US/10087013	*** 1 standard deviation above mean *** *** 0 standard deviation from mean ***	308	7	43	-0.58	0
3. US-10-087-013-9 Sequence 9, Application US/10087013	*** 1 standard deviation above mean *** *** 0 standard deviation from mean ***	351	7	46	-0.58	0

Initial Score	Optimized Score	Significance	Residue Identity	Matches	Mismatches	Gaps	Conservative Substitutions
1. US-10-087-013-2 (1-345)	7	43	21%	64	160	0	69
US-10-087-013-11 Sequence 11, Application US/10087013	7	43	21%	64	160	0	69


```

2. US-10-087-013-2 (1-345)
US-10-087-013-11 Sequence 11, Application US/10087013
Initial Score = 7 Optimized Score = 43 Significance = -0.58
Residue Identity = 21% Matches = 64 Mismatches = 160
Gaps = 69 Conservative Substitutions = 0
70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310
DKGIRYRSEYCOVCPDGCYKCGIKYTKHSNDREVRNEDYKPPGKVPNTIYLSG-----NEO
GNDG-----SNEISGCNPKESY-PMDCK-KNIDNSHSGACMPPRKLCV
RDLTGGELIRKPEDILTKFNCAKETHFAMHYK-----KDNVAENELSGKI---PEGFRKOMYTF
GDTG-----KLENFCSSTNYKDKNNQKKECYKIDENIRCKLEONTETLNNDPKIISHNFEELWYLL
RDITKNNDKLTKCINNTTHCIDECAKNCCLCPDRWYKQKEEENSTIKLPT---KKNIQOYSTNINNIFE
GD---PRD-----IFGCT--DISSC-RYIKDTSQITKSLGDDATTEKGDTHDDNNKLOEMWTHIQPKIME
110 120 130 140 150 160

```


> 0 <
01 10 IntelIGenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file pepb3.res made by shanley on Tue 24 Jun 103 9:03:02-PDT

Query sequence being compared:	U39215.1 (1-273)
Number of sequences searched:	3
Number of scores above cutoff:	3

Results of the initial comparison of PEPB.PEP (1-276) with:
File : pep911.pep

[illegible]

PARAMETERS

	Unary	K-tuple Joining penalty Window size
Similarity matrix	1	3
Mismatch penalty	1.00	20
Gap penalty	0.05	276
Gap size penalty	1	
Cutoff score	0	
Randomization group		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	24	23	4.04

Times:	CPU	Total Elapsed
0.000000	0.000000	0.000000

Number of residues: 970

Number of scores above cutoff: 3

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Int.	Opt.	Length	Score	Score	Sig.	Frame

	****	1	standard deviation	above mean	****
1. US-10-087-013-9 Sequence 9, Application US	351	29	112	1.24	0
2. US-10-087-013-11 Sequence 11, Application	308	22	105	-0.49	0
3. US-10-087-013-10 Sequence 10, Application	311	22	106	-0.49	0

1. PEPB.PEP (1-276)
US-10-087-013-9, **sequence 9**, Application US/10087013

Initial Score	=	29	Optimized Score	=	112	Significance	=	1.24
Residue Identity	=	41%	Matches	=	125	Mismatches	=	137
Gaps	=	39	Conservative Substitutions	=			=	0

X 10 20 30 40 50
DHPKK-----NSNGYPD--WCGNINLVEDPVCMPRRQKLCVHFLANDNETIKKIQQSOV
| |
PCMYVKQLISEQIEKNKHNCRTEDAKMKCEKTKLGDEGVCMPRRQLCVHYLTKLNDSSK---EE

X' 10 20 30 40 50 60

60 70 80 90 100 110 120
 NLKEAFITKAAAEETFFSWYKYKSDGEGNELDKLKGKGPAPAFLRSMETFDGYDPLFTGDIS--KGHGE
 DEEATITTT
 DLEEAFTKSAAEETFLIROYNSK--NVEDDKLIHDMIPPEEFRRMFTFDGYDCLDLDISEKLTADHD
 70 80 90 100 110 120 130

130 140 150 160 170 180
GSKLKQIDSLFNGDOKSPNCK---TQEWMTSHSEIIEAMICAL-VIGAKRD---PFGNYGNVKE
VTTAKKKTIAVQKIGSKTNNKKYLLEREGMKKRYGSLINKGHCALSYTEPKKDEGVRIYLRK-IYNNK
140 150 160 170 180 190 200

```

190      210      220      230      240      250      260
SDKSTTLEEFARPOFLRLEEMWDYCYTQOYLKIDYQKCSNDQLKDCFNKCKDGYAKKKREWJ
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
210      220      230      240      250      260      270
NDIKETLEEFASPPFLRIRVMEGSDFYKNNKKELYSLLKKKCS-CTLRNNGNSNTODNENCGACK--T

```

2/0 X
PQDKYYK-DEDRKKRF
|| | | |
QCEYKKWMERKKHYSSQKKKFLYKNSATYNNGL
280 290 300 310

2. PEPB.PEP (1-276)
US-10-087-013-11 **Sequence 11**, Application US/10087013

Initial Score	=	22	Optimized Score	=	105	Significance	=	-0.49
Residue Identity	=	40%	Matches	=	118	Mismatches	=	146
Gaps	=	31	Conservative Substitutions	=			=	0

DCHPRKKNINFLVEDRVCMPRRORCLAFHANEIKTKLOSIVNLEKAFISK
 | | | | | | | | | | | | | | | | | |
 GNDGNSIEIGSNPK---ESYPRMDCKKIINDSHSGACAMPRRORCLCYRDLTGGGEIRK---PEDILTFIFNIC
 | | | | | | | | | | | | | | | | | |
 10 20 30 40 50 60

70
 80
 90
 100
 110
 120
 130
 AAATETFSWYKRSKDGEENELDKELGKIPAFALSMFYETGDDVDFPTGDIS-- --KGHEGSKLEKE
 AAEETTFHFAHKKYK-KDNVAE--NELKSGKIPEGFRMWTYTGDFDFDIFEGDISSCRYIKDTQSITKSKL

QIDSLEKRNDOQSPNGKTRQEWMTHEHETIEALCAL--VKIGAKKDDTEYVCGNNKFSDK-STTLEEF
140 150 160 170 180 190
GDOATTEKGDTHIDNNKILQEWMTIHGPRTWEGKLCALTNGLSESEKNNLLODYSYNNKLNNAEKDDCLEFF
140 150 160 170 180 200

260 270 X
K---KEWIPQDKYY---KD--ERDKRR
| | | | |
KGKFADEKITDKEGYEGFSTKDASEYLKKK
290 300 310